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MICROBIAL METHYLATION OF MERCURY IN ACID STRESSED LAKES - ROLE OF SULPHATE REDUCING BACTERIA

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INTRODUCTION

Elevated levels of mercury have recently been detected in fish from acid stressed and other softwater contain sport fish that are above the guideline for unrestricted human consumption. There is no clear source point source mercury contamination in this area and thus no abatement measures have been implemented. This non-combustion sources.

Some of the occurrences of the elevated mercury levels in fish tissue, in lakes removed from point & MacCrimmon, 1933; Bjorkland et al., 1984; Suns et al., 1987; Hakanson et al., 1988). Other factors, such as the supply of organic carbon (Bodaly et al., 1984; Hecky et al., 1987; Jackson, 1988), the form and savailability of mercury (Rudd & Turner, 1983), the presence of humic and fulvic acids (Mannio et al., 1986; had the amount of sulphate present (Compeau & Bartha, 1985; Gilmour & Mitchell, in press), are also statistically related to the level of fish mercury.

Mercury readily accumulates in muscle as well as other tissue of fish and is biomagnified in the aquatic food chain (Huckabee et al., 1979). Methylation of mercury by microgranisms produces a form of mercury that is more toxic and more biologically available to biota than is inorganic mercury (Beijer & Iogically, factors which change or stimulate portions of this communities on lake sediment are known to methylate inorganic mercury and (Summers & Silver, 1978). It has been suggested, based on estuarine studies, that one group of sediment 1985). It was previously proposed that methanogenic bacteria were responsible for the major amount of mercury methylation (Wood et al., 1968; Jensen & Jernelov, 1968).

The increased input of sulphate from acidic deposition may stimulate sulphate-reducing bacteria over the other sediment populations thereby potentially increasing the rate of methylmercury production in the system. The objective of our study was to elucidate the possible role of freshwater sulphate-reducing bacteria role with sulphate input can have on their activity. The methylmercury production was examined by adding specific microbial inhibitors to anoxic lake sediments spiked with sulphate reducion rate and methylation of mercury was examined by adding appropriate ranges of concentrations of sulphate to sulphate to sulphate to sulphate reducing bacteria both in

MATERIALS AND METHODS

Dickie Lake in the Muskoka-Haliburton region of south-central Ontario, Canada (Latitude 45° 09°N, Longitude 79° 05°W) was sampled regularly to provide sediment and water. The pH of the lake ranged from content (Loss on Ignition, 450°C for 4 hrs, was 1-4%) and the lake water had a sulphate concentration of 6-8

Sediments were collected from the epilimnion near the outflow of Dickie lake. Cores (10 by 50 cm) were taken by hand at a depth of 1-2 m in replicates of six. The cores were then packed on ice and extruded and manipulated in an anaerobic glove box filled with flowing oxygen-free nitrogen gas. After the 10 cm of floc had been removed, the subsequent 5-10 cm sof anoxic sediments were pooled from at least acid sensitive lakes in the study area, Muskoka medium (Wehr and Brown, 1985), with the following modifications: sulphate content was lowered to 3 mg.L.¹, vitamins were eliminated, and 0.5 g.L.¹ of yeast oxygen catract was added. A slurry was made of 1 part sediment to 3 parts Muskoka medium. Gr. L. and aliquots were dispensed into 60 ml serum bottles and sealed with butyl rubber stoppers (Compeau and Bartha, 1985).

All reagents were then added by syringe into the sealed bottles outside the anaerobic glove box through the respective septa.

Specific rates of mercury methylation were determined using the radiochemical method of Furutani and Rudd (1980). 1 µCi of ²⁰HgCl₂, approximately 1 µg of Hg, was added to each 40 ml sample bottle through the septum (approx. 67 ng per dry sediment) and incubated at 25°C. At the end of the experiment, 1 ml of 4N HCl was added to stop the biological reaction and alkylated ²⁰Hg was extracted from the total contents of the bottle (Furutani and Rudd, 1980). The alkylated ²⁰Hg, extracted into toluene, was then dried with Na₂SO, to remove excess water and determined on a gamma counter. All experiments were done with at least 3 replicates at each condition along with three acid-killed blanks (1 ml of 4N HCl added to bottle). The extraction efficiency of the technique was assessed by using the methylated isotope, CH₂²⁰Hg; extraction was 78-80% efficient. All calculations were corrected accordingly.

RESULTS & DISCUSSION

Both sulphate-reducing bacteria and methanogens were present in the anoxic sediment of Dickie Lake. Specific microbial inhibitors, that were added to ²⁰⁰Hg spiked slurries, were effective in inhibiting the target microbial population, i.e. NaMoO, inhibited sulphate-reducing bacteria and BESA inhibited methanogenic bacteria. NaMoO, decreased methyl-mercury production by 75% but BESA did not significantly decrease methyl-mercury production (Figure 1). Varying levels of inhibitors; 5, 10, 20 mM NaMo and 7.5, 15, 30 mM BESA, produced the same pattern as shown in Figure 1 independent of concentration. This indicates that sulphate-reducing bacteria are the main methylators of mercury in these sediments under the experimental conditions that are used.

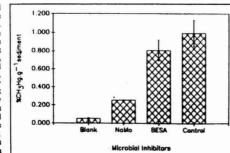


Figure 1. Production of CH₃²⁰⁰Hg in anoxic sediment slurries (Blank = Acid killed, NaMo = 10 mM Na₂MoO₄, BESA = 15 mM 2-Bromoethane sulfonic acid, Control = no additions).

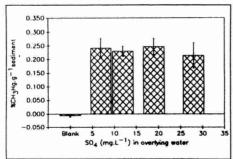


Figure 2. Production of CH₃²⁸⁵Hg in anoxic sediment slurries over the naturally occurring range of sulphate levels found in the experimental area.

The rate of sulphate reduction from the water overlying the sediment slurries increased as the concentration of sulphate in the water increased. This indicates that the resident population of sulphate-reducing bacteria are stimulated by small inputs in sulphate to the water column. However, the increase in activity of the sulphatereducers did not correlate increased production rates of methylmercury. Across the range of sulphate concentrations tested, there was no significant difference in the amount of methylmercury produced (Figure 2). Therefore the stimulatory effect of sulphate on these bacteria does not seem to be translated into increased methylation rates of mercury.



CONCLUSIONS

Under our experimental conditions, sulphate-reducing bacteria do appear to be major methylators of However, the stimulatory effect of sulphate, within normal levels, on these bacteria's ability to further methylate mercury remains unclear.

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